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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/963,656DATE: 03/13/98
TIME: 16:53:52

INPUT SET: S24138.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Gerard, Craig J.
6 Gerard, Norma P.
7 Mackay, Charles R.
8 Ponath, Paul D.
9 Post, Theodore W.
10 Qin, Shixin
11
12 (ii) TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
13 ANTAGONISTS THEREOF
14
15 (iii) NUMBER OF SEQUENCES: 18
16
17 (iv) CORRESPONDENCE ADDRESS:
18 (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
19 (B) STREET: Two Militia Drive
20 (C) CITY: Lexington
21 (D) STATE: MA
22 (E) COUNTRY: USA
23 (F) ZIP: 02173
24
25
26 (v) COMPUTER READABLE FORM:
27 (A) MEDIUM TYPE: Floppy disk
28 (B) COMPUTER: IBM PC compatible
29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
31
32
33 (vi) CURRENT APPLICATION DATA:
34 (A) APPLICATION NUMBER:
35 (B) FILING DATE: 03-NOV-1997
36 (C) CLASSIFICATION:
37
38 (vii) PRIOR APPLICATION DATA:
39 (A) APPLICATION NUMBER: 08/720,565
40 (B) FILING DATE: 30-SEP-1996
41
42 (vii) PRIOR APPLICATION DATA:
43 (A) APPLICATION NUMBER: PCT/US96/00608
44 (B) FILING DATE: 19-JAN-1996
45
46 (vii) PRIOR APPLICATION DATA:

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47 (A) APPLICATION NUMBER: US 08/375,199
48 (B) FILING DATE: 19-JAN-1995
49

50
51 (viii) ATTORNEY/AGENT INFORMATION:
52 (A) NAME: Brook, David E.
53 (B) REGISTRATION NUMBER: 22,592
54 (C) REFERENCE/DOCKET NUMBER: LKS94-05A2Z
55

56 (ix) TELECOMMUNICATION INFORMATION:
57 (A) TELEPHONE: 781-861-6240
58 (B) TELEFAX: 781-861-9540

59 (2) INFORMATION FOR SEQ ID NO:1:
60

61 (i) SEQUENCE CHARACTERISTICS:
62 (A) LENGTH: 1689 base pairs
63 (B) TYPE: nucleic acid
64 (C) STRANDEDNESS: double
65 (D) TOPOLOGY: linear
66

67 (ii) MOLECULE TYPE: DNA (genomic)
68
69
70

71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
72

73	AATCCTTTTC CTGGCACCTC TGATATCCTT TTGAAATTCA TGTAAAGAA TCCCTAGGCT	60
74		
75	GCTATCACAT GTGGCATCTT TGTTGAGTAC ATGAATAAAT CAACTGGTGT GTTTTACGAA	120
76		
77	GGATGATTAT GCTTCATTGT GGGATTGTAT TTTTCTTCTT CTATCACAGG GAGAAGTGAA	180
78		
79	ATGACAACCT CACTAGATAC AGTTGAGACC TTTGGTACCA CATCCTACTA TGATGACGTG	240
80		
81	GGCCTGCTCT GTGAAAAAGC TGATACCAGA GCACTGATGG CCCAGTTTGT GCCCCCCTG	300
82		
83	TACTCCCTGG TGTTCACTGT GGGCCTCTTG GGCAATGTGG TGGTGGTGAT GATCCTCATA	360
84		
85	AAATACAGGA GGCTCCGAAT TATGACCAAC ATCTACCTGC TCAACCTGGC CATTTCCGAC	420
86		
87	CTGCTCTTCC TCGTCACCCT TCCATTCTGG ATCCACTATG TCAGGGGGCA TAACTGGGTT	480
88		
89	TTTGGCCATG GCATGTGTAA GCTCCTCTCA GGGTTTTATC ACACAGGCTT GTACAGCGAG	540
90		
91	ATCTTTTTCA TAATCCTGCT GACAATCGAC AGGTACCTGG CCATTGTCCA TGCTGTGTTT	600
92		
93	GCCCTTCGAG CCCGGACTGT CACTTTTGGT GTCATCACCA GCATCGTCAC CTGGGGCCTG	660
94		
95	GCAGTGCTAG CAGCTCTTCC TGAATTTATC TTCTATGAGA CTGAAGAGTT GTTTGAAGAG	720
96		
97	ACTCTTTGCA GTGCTCTTTA CCCAGAGGAT ACAGTATATA GCTGGAGGCA TTTCCACACT	780
98		
99	CTGAGAATGA CCATCTTCTG TCTCGTTCTC CCTCTGCTCG TTATGGCCAT CTGCTACACA	840

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100
101 GGAATCATCA AAACGCTGCT GAGGTGCCCC AGTAAAAAAA AGTACAAGGC CATCCGGCTC 900
102
103 ATTTTGTGCA TCATGGCGGT GTTTTTCATT TTCTGGACAC CCTACAATGT GGCTATCCTT 960
104
105 CTCTCTTCCT ATCAATCCAT CTTATTTGGA AATGACTGTG AGCGGACGAA GCATCTGGAC 1020
106
107 CTGGTCATGC TGGTGACAGA GGTGATCGCC TACTCCCACT GCTGCATGAA CCCGGTGATC 1080
108
109 TACGCCTTTG TTGGAGAGAG GTTCCGGAAG TACCTGCGCC ACTTCTTCCA CAGGCACTTG 1140
110
111 CTCATGCACC TGGGCAGATA CATCCCATT CTTCTAGTG AGAAGCTGGA AAGAACCAGC 1200
112
113 TCTGTCTCTC CATCCACAGC AGAGCCGGAA CTCTCTATTG TGTTTTAGGT AGATGCAGAA 1260
114
115 AATTGCCTAA AGAGGAAGGA CCAAGGAGAT NAAGCAAACA CATTAAGCCT TCCACACTCA 1320
116
117 CCTCTAAAC AGTCCTTCAA ACCTTCCAGT GCAACACTGA AGCTCTTAAG AACTGAAAT 1380
118
119 ATACACACAG CAGTAGCAGT AGATGCATGT ACCCTAAGGT CATTACCACA GGCCAGGGCT 1440
120
121 GGGCAGCGTA CTCATCATCA ACCTAAAAAG CAGAGCTTTG CTTCTCTCTC TAAAATGAGT 1500
122
123 TACCTATATT TTAATGCACC TGAATGTTAG ATAGTTACTA TATGCCGCTA CAAAAGGTA 1560
124
125 AAACCTTTTTA TATTTTATAC ATTAACCTCA GCCAGCTATT ATATAAATAA AACATTTTCA 1620
126
127 CACAATACAA TAAGTTAACT ATTTTATTTT CTAATGTGCC TAGTTCTTTC CCTGCTTAAT 1680
128
129 GAAAAGCTT 1689
130
131
132

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr
1 5 10 15
Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu
20 25 30
Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Phe Gly

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	35	40	45
153			
154			
155	Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg		
156	50	55	60
157			
158	Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp		
159	65	70	75 80
160			
161	Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly		
162		85 90	95
163			
164	His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe		
165		100 105	110
166			
167	Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr		
168		115 120	125
169			
170	Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala		
171		130 135	140
172			
173	Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu		
174		145 150	155 160
175			
176	Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu		
177		165 170	175
178			
179	Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val		
180		180 185	190
181			
182	Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu		
183		195 200	205
184			
185	Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys		
186		210 215	220
187			
188	Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu		
189		225 230	235 240
190			
191	Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn		
192		245 250	255
193			
194	Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp		
195		260 265	270
196			
197	Cys Glu Arg Thr Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val		
198		275 280	285
199			
200	Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val		
201		290 295	300
202			
203	Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu		
204		305 310	315 320
205			

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206 Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
207 325 330 335
208
209 Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
210 340 345 350
211
212 Ile Val Phe
213 355
214
215
216

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 92..1156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

234
235 TTGTGCTTAT CCGGGCAAGA ACTTATCGAA ATACAATAGA AGACCCACGC GTCCGGTTTT 60
236
237 TACTTAGAAG AGATTTTCAG GGAGAAGTGA A ATG ACA ACC TCA CTA GAT ACA 112
238 Met Thr Thr Ser Leu Asp Thr
239 1 5
240
241 GTT GAG ACC TTT GGT ACC ACA TCC TAC TAT GAT GAC GTG GGC CTG CTC 160
242 Val Glu Thr Phe Gly Thr Thr Ser Tyr Tyr Asp Asp Val Gly Leu Leu
243 10 15 20
244
245 TGT GAA AAA GCT GAT ACC AGA GCA CTG ATG GCC CAG TTT GTG CCC CCG 208
246 Cys Glu Lys Ala Asp Thr Arg Ala Leu Met Ala Gln Phe Val Pro Pro
247 25 30 35
248
249 CTG TAC TCC CTG GTG TTC ACT GTG GGC CTC TTG GGC AAT GTG GTG GTG 256
250 Leu Tyr Ser Leu Val Phe Thr Val Gly Leu Leu Gly Asn Val Val Val
251 40 45 50 55
252
253
254
255 GTG ATG ATC CTC ATA AAA TAC AGG AGG CTC CGA ATT ATG ACC AAC ATC 304
256 Val Met Ile Leu Ile Lys Tyr Arg Arg Leu Arg Ile Met Thr Asn Ile
257 60 65 70
258

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SEQUENCE VERIFICATION REPORT
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